

FIG. 1A

Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
1 5 10 15

Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
20 25 30

Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
35 40 45

Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
50 55 60

Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
65 70 75 80

Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
85 90 95

Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
100 105 110

Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
115 120 125

Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
130 135 140

Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser
145 150 155 160

Asn Glu Ile Val Glu Lys Leu Leu Arg Arg Lys Phe Ile Pro Asp
165 170 175

Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr
180 185 190

His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn
195 200 205

Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu
210 215 220

Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr
225 230 235 240

Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln
245 250 255

Ala Glu Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala
260 265 270

Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala
275 280 285

Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln
290 295 300

FIG. 1B

Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu
305 310 315 320

Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln
325 330 335

His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu
340 345 350

Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn
355 360 365

Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His
370 375 380

Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu
385 390 395 400

Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
405 410 415

Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
420 425 430

Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
435 440 445

Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
450 455 460

Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
465 470 475 480

Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
485 490 495

Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
500 505 510

Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
515 520 525

Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
530 535 540

Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
545 550 555 560

Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
565 570 575

Val Thr Ile Asn Ala Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
580 585 590

Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu
595 600

FIG. 2A

GTCCAGGAAC TCCTCAGGAG CGCCTCTTC AGCTCACAG CCAGACGCC TCAGACAGCA 60
AAGGCTACCC CGCGCCCCCG CCCTGCGCGC CGCTGCGATG CTGCGCGCG CGCTGCTGCT 120
GTCCGGGTC CTGGCGCTCA GCCATACAGC AAATCCTTGC TGTCCCCACC CATGTCAAA 180
CCGAGGTGTA TGTATGAGTG TGGGATTGAA CCAGTATAAG TCGGATTGTA CCCGGACAGG 240
ATTCTATGGA GAAAATGCT CAACACCGGA ATTCTTGACA AGAATAAAAT TATTTCTGAA 300
ACCCACTCCA AACACACGTC ACTACATACT TACCCACTTC AAGGGATTT GGAACGTG 360
GAATAACATT CCCTTCCTTC GAAATGCAAT TATGAGTTAT GTGTTGACAT CCAGATCACA 420
TTTGTGAC AGTOCACCAA CTTACAATGC TGACTATGGC TACAAAAGCT GGGAGCCTT 480
CTCTAACCTC TCCTATTATA CTAGAGCCCT TCCTCTGTC CCTGATGATT GCGGACTCC 540
CTGGGTGTC AAAGGTAAAA AGCAGCTTC TGATTCAAAAT GAGATTGTCG AAAAATTGCT 600
TCTAAGAAGA AAGTTCATCC CTGATCCCCA GGGCTAAAC ATGATTTG CATTCTTGC 660
CCAGCACTTC ACAGCACCAGT TTTCAGAC AGATCATAAG CGAGGGCCAG CTTTACCAA 720
CGGGCTGGGC CATGGGGTGG ACTTAAATCA TATTTACGGT GAAACTCTGG CTAGACAGG 780
TAAACTGCGC CTTTCAAGG ATGGAAAAT GAAATATCAG ATAATTGATG GAGAGATGTA 840
TCCTCCCACA GTCAAAGATA CTCAGGCAGA GATGATCTAC CCTCTCAAG TCCCTGAGCA 900
TCTACGGTT GCTGTGGGGC AGGAGGTCTT TGGCTGCTG CCTGGCTGA TGATGTATGC 960
ACAATCTGG CTGGGGAAAC ACAACAGAGT ATGTGATGTC CTTAACACGG AGCATCCTGA 1020
ATGGGGTGT GAGCAATTGT TCCAGACAAG CAGGCTATAA CTGATAGGAG AGACTATTAA 1080
GATTGTGATT GAAGATTATG TGCAACACTT GAGTGGCTAT CACTTCAAAC TGAAATTGTA 1140
CCCAGAACTA CTTTCAACA AACAACTCCA GTACCAAAAT CGTATTGCTG CTGAATTAA 1200
CACCCCTAT CACTGGCATC CCTCTGCTG TGACACCTTT CAAATTCTAG ACCAGAAATA 1260
CAACTATCAA CAGTTATCT ACAACAACTC TATATTGCTG GAACATGGAA TTACCCAGTT 1320
TGTGAATCA TTCACCAGGC AAATTGCTGG CAGGGTTGCT GGTGGTAGGA ATGTTCCACC 1380
CGCAGTACAG AAAGTATCAC AGGCTCCAT TGACCAGAGC AGGCAGATGA AATACCACTC 1440
TTTAATGAG TACCGCAAAC GCTTATGCT GAAGCCCTAT GAATCATTTG AAGAACTTAC 1500
AGGAGAAAAG GAAATGCTG CAGAGTTGGA AGCACTCTAT GGTGACATCG ATGCTGTGGA 1560
GCTGTATCTT GCGCTCTGG TAGAAAAGCC TCGGCCAGAT GCCATCTTGC GTGAAACCAT 1620
GGTAGAAGTT GGAGCACCAT TCTCTGAA AGGACTTATG GGTAAATGTTA TATGTTCTCC 1680
TGCCTACTGG AAGCCAAGCA CTTTGGTGG AGAAGTGGGT TTCAAAATCA TCAACACTGC 1740

FIG. 2B

CTCAATTAG TCTCTCATCT GCAATAACGT GAAGGGCTGT CCCTTACCTT CATTAGTGT 1800
TCCAGATCCA GAGCTCAITA AAACAGTCAC CATCAATGCA AGTCTTCCOC GCTCCGGACT 1860
AGATGATATC AATGCCACAG TACTACTAAA AGAACGGTCG ACTGAACGTG AGAACGCTA 1920
TGATCATATT TATTTATTTA TATGAACCAT GTCTATTAAAT TTAATTATTT AATAATATT 1980
ATATTAAACT CCTTATGTTA CTTAACATCT TCTGTAACAG AAGTCAGTAC TCTGTGCG 2040
GAGAAAGGAG TCATACTTGT GAAGACCTTT ATGTCACTAC TCTAAAGATT TTGCTGTTCC 2100
TGTAAAGTTT GGAAAACAGT TTTTATCTG TTTTATAAAC CAGAGAGAAA TGAGTTTGA 2160
CGTCTTTTA CTGAAATTC AACTTATATT ATAAGGACGA AAGTAAAGAT GTTGAATAC 2220
TTAAACACTA TCACAAGATG CCAAAATCT GAAAGTTTT ACACTGTCGA TGTTCCAAT 2280
GCATCTCCA TGATGCATTA GAAGTAACTA ATGTTGAAA TTTAAAGTA CTTTGGGTA 2340
TTTTCTGTC ATCAACAAA ACACGTATCA GTGCATTATT AAATGAATAT TTAAATTAGA 2400
CATTACCACT AATTCATGT CTACTTTTA AAATCAGCAA TGAAACAATA ATTTGAAATT 2460
TCTAAATTCA TAGGGTAGAA TCACCTGTAAC AAGCTGTTT GATTTCTTAA AGTTATTAAA 2520
CTTGTACATA TACCAAAAG AAGCTGTCCT GGATTTAAAT CTGAAAATC AGATGAAATT 2580
TTACTACAAT TGCTGTTAA AATATTITAT AAGTGTGTT CCTTTTCAC CAAGAGTATA 2640
AACCTTTTA GTGTGACTGT TAAAACCTCC TTTAAATCA AAATGCCAAA TTATTAAGG 2700
TGGTGGAGCC ACTGCAGTGT TATCTAAAA TAAGAATATC CTGTTGAGAT ATTCAGAAAT 2760
CTGTTATAT GGCTGTAAC ATGTAACACCC CCCATAACCC CGCCAAAAGG GGTCCTACCC 2820
TTGAACATAA AGCAATAACC AAAGGAGAAA AGCCAAATT ATGGTCCA AATTAGGGT 2880
TTAAACTTTT TGAAGCAAAC TTTTTTTAG CCTTGTGAC TGCAACCTG GTACTCAGAT 2940
TTTGTATGA GGTTAATGAA GTACCAAGCT GTGCTGAAT AACGATATGT TTTCTCAGAT 3000
TTTCTGTTGT ACAGTTAAT TTACCACTCC ATATCACATT GCAAAAGTAG CAATGACCTC 3060
ATAAAATACC TTTCAAAAT GCTTAAATTC ATTCACACCA TTAAATTAT CTCAGTCTG 3120
AAGCCAATTIC AGTAGGTGCA TTGGAATCAA GCGTGGCTAC CTGCAATGCTG TTCTTTCT 3180
TTTCTCTTT TAGCCATTIT GCTAAGAGAC ACAGTCTCT CAAACACTTC GTTCTCCTA 3240
TTTGTTTTA CTAGTTTAA GATCAGAGIT CACTTTCTT GGACTCTGCC TATATTITCT 3300
TACCTGAACT TTGCAAGIT TTCAAGTAAA CCTCAGCTCA GGACTGCTAT TTAGCTCCTC 3360
TTAAGAAGAT TAAAAAAA AAAAAAG 3387